

SEQUENCE LISTING

<110> Wu, Hongjiang
Crooke, Stanley T.

<120> Human RNase III And Compostions And Uses Thereof

<130> ISIS5029/ISPH-0522

<140> 09/900,425

<141> 2001-07-06

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<170> PatentIn version 3.1

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Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
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Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
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Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
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Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
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Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Val Met

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| His | Arg | Ser | Pro | Ser | Arg | Glu | Lys | Lys | Arg | Ala | Arg | Trp | Glu | Glu | Glu |
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Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
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Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
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Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
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Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile
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Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
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Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
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Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
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Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
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| Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His 1105 1110 1115 1120 | | |
| Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn 1125 1130 1135 | | |
| His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser 1140 1145 1150 | | |
| Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp 1155 1160 1165 | | |
| His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn 1170 1175 1180 | | |
| Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala 1185 1190 1195 1200 | | |
| Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu Arg Thr Lys Thr 1205 1210 1215 | | |
| Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu Tyr Thr Asp Lys 1220 1225 1230 | | |
| Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys Phe Phe Pro Arg 1235 1240 1245 | | |
| Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp Pro Lys Ser Gln 1250 1255 1260 | | |
| Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly Lys Glu Pro Asp 1265 1270 1275 1280 | | |
| Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro Ser His Ala Arg 1285 1290 1295 | | |

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Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln Lys Arg Phe Ile
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Thr Leu Ala Lys Asn Cys Arg Ile Asp Glu Met Leu Gln Tyr Ser His
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Gly Ala Asp Leu Ile Asn Val Ala Glu Phe Lys His Ala Leu Ala Asn
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Ala Phe Glu Ala Val Met Ala Ala Ile Tyr Leu Asp Gly Gly Leu Ala
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Pro Cys Asp Val Ile Phe Ser Lys Ala Met Tyr Gly His Gln Pro Val
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Leu Lys Glu Lys Trp Asp His Ile Asn Glu His Glu Leu Lys Arg Glu
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Asp Pro Gln Gly Asp Arg Asp Leu Ser Phe Ile Thr Pro Thr Leu Ser
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Thr Phe His Ala Leu Glu Glu Arg Leu Gly Ile Gln Phe Asn Asn Ile
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Arg Leu Leu Ala Lys Ala Phe Thr Arg Arg Asn Ile Pro Asn Asn Asp
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Leu Thr Lys Gly His Asn Gln Arg Leu Glu Trp Leu Gly Asp Ser Val
 195 200 205

Leu Gln Leu Ile Val Ser Asp Phe Leu Tyr Arg Arg Phe Pro Tyr His
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His Glu Gly His Met Ser Leu Leu Arg Thr Ser Leu Val Ser Asn Gln
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Thr Gln Ala Val Val Cys Asp Asp Leu Gly Phe Thr Glu Phe Val Ile
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Lys Ala Pro Tyr Lys Thr Pro Glu Leu Lys Leu Lys Asp Lys Ala Asp
 260 265 270

Leu Val Glu Ala Phe Ile Gly Ala Leu Tyr Val Asp Arg Gly Ile Glu
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His Cys Arg Ala Phe Ile Arg Ile Val Phe Cys Pro Arg Leu Lys His
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Phe Ile Glu Ser Glu Lys Trp Asn Asp Ala Lys Ser His Leu Gln Gln
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Trp Cys Leu Ala Met Arg Asp Pro Ser Ser Ser Glu Pro Asp Met Pro
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Glu Tyr Arg Val Leu Gly Ile Glu Gly Pro Thr Asn Asn Arg Ile Phe
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Lys Ile Ala Val Tyr Tyr Lys Gly Lys Arg Leu Ala Ser Ala Ala Glu
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Ser Asn Val His Lys Ala Glu Leu Arg Val Ala Glu Leu Ala Leu Ala
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Ile Arg Lys Leu Met Phe Ala Met Lys Ala Leu Leu Glu Glu Thr Lys
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His Ser Thr Lys Asp Asp Val Asn Leu Val Ile Pro Gly Ser Thr Trp
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Ser His Ile Glu Gly Val Tyr Glu Met Leu Lys Ser Arg His Asp Arg
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Gln Asn Glu Pro Val Ile Glu Glu Pro Ser Ser His Pro Lys Asn Gln
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Lys Asn Gln Glu Asn Asn Glu Pro Thr Ser Glu Glu Phe Glu Glu Gly
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Glu Tyr Pro Pro Pro Leu Pro Pro Leu Arg Ser Glu Lys Leu Lys Glu
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Gln Val Phe Met His Ile Ser Arg Ala Tyr Glu Ile Tyr Pro Asn Gln
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Ser Asn Pro Asn Glu Leu Leu Asp Ile His Asn Glu Arg Leu Glu Phe
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Leu Gly Asp Ser Phe Phe Asn Leu Phe Thr Thr Arg Ile Ile Phe Ser
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Lys Phe Pro Gln Met Asp Glu Gly Ser Leu Ser Lys Leu Arg Ala Lys
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Asp Lys Thr Leu Val Leu Ser Tyr Ser Ala Glu Lys Asp Gln Leu Arg
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Lys Ser Gln Lys Val Ile Ala Asp Thr Phe Glu Ala Tyr Leu Gly Ala
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Leu Ile Leu Asp Gly Gln Glu Glu Thr Ala Phe Gln Trp Val Ser Arg
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Leu Leu Gln Pro Lys Ile Ala Asn Ile Thr Val Gln Arg Pro Ile Asp
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Lys Leu Ala Lys Ser Lys Leu Phe His Lys Tyr Ser Thr Leu Gly His
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Glu Gly Tyr Val Ile Ala Cys Ile Phe Asn Gly Lys Glu Val Ala Arg
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Asn Asn Gln Asp Arg Val Pro Val Gln Ile Leu Pro Ser Leu Ser Arg
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Tyr Gln Leu Lys Leu Ala Ala Glu Leu Lys Thr Leu His Asp Leu Lys
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Lys Asp Ala Ile Leu Thr Glu Ile Thr Asp Tyr Glu Asn Glu Phe Asp
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Thr Glu Gln Lys Gln Pro Ile Leu Gln Glu Ile Ser Lys Ala Asp Met
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Glu Lys Leu Glu Lys Leu Glu Gln Val Lys Arg Glu Lys Arg Glu Lys
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Glu Asp Glu Gly Glu Asp Ser Tyr Asp Pro Thr Lys Ala Gly Asp Ile
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Val Lys Ala Thr Lys Trp Pro Pro Lys Leu Pro Glu Ile Gln Asp Leu
 195 200 205

Ala Ile Arg Ala Arg Val Phe Ile His Lys Ser Thr Ile Lys Asp Lys
210 215 220

Val Tyr Leu Ser Gly Ser Glu Met Ile Asn Ala His Asn Glu Arg Leu
225 230 235 240

Glu Phe Leu Gly Asp Ser Ile Leu Asn Ser Val Met Thr Leu Ile Ile
245 250 255

Tyr Asn Lys Phe Pro Asp Tyr Ser Glu Gly Gln Leu Ser Thr Leu Arg
260 265 270

Met Asn Leu Val Ser Asn Glu Gln Ile Lys Gln Trp Ser Ile Met Tyr
275 280 285

Asn Phe His Glu Lys Leu Lys Thr Asn Phe Asp Leu Lys Asp Glu Asn
290 295 300

Ser Asn Phe Gln Asn Gly Lys Leu Lys Leu Tyr Ala Asp Val Phe Glu
305 310 315 320

Ala Tyr Ile Gly Gly Leu Met Glu Asp Asp Pro Arg Asn Asn Leu Pro
325 330 335

Lys Ile Arg Lys Trp Leu Arg Lys Leu Ala Lys Pro Val Ile Glu Glu
340 345 350

Ala Thr Arg Asn Gln Val Ala Leu Glu Lys Thr Asp Lys Leu Asp Met
355 360 365

Asn Ala Lys Arg Gln Leu Tyr Ser Leu Ile Gly Tyr Ala Ser Leu Arg
370 375 380

Leu His Tyr Val Thr Val Lys Lys Pro Thr Ala Val Asp Pro Asn Ser
385 390 395 400

Ile Val Glu Cys Arg Val Gly Asp Gly Thr Val Leu Gly Thr Gly Val
405 410 415

Gly Arg Asn Ile Lys Ile Ala Gly Ile Arg Ala Ala Glu Asn Ala Leu
420 425 430

Arg Asp Lys Lys Met Leu Asp Phe Tyr Ala Lys Gln Arg Ala Ala Ile
435 440 445

Pro Arg Ser Glu Ser Val Leu Lys Asp Pro Ser Gln Lys Asn Lys Lys
450 455 460

Arg Lys Phe Ser Asp Thr Ser
465 470

<210> 6
<211> 226
<212> PRT
<213> Escherichia coli

<400> 6

Met Asn Pro Ile Val Ile Asn Arg Leu Gln Arg Lys Leu Gly Tyr Thr
1 5 10 15

Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
20 25 30

Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
35 40 45

Ser Tyr Val Ile Ala Asn Ala Leu Tyr His Arg Phe Pro Arg Val Asp
50 55 60

Glu Gly Asp Met Ser Arg Met Arg Ala Thr Leu Val Arg Gly Asn Thr
65 70 75 80

Leu Ala Glu Leu Ala Arg Glu Phe Glu Leu Gly Glu Cys Leu Arg Leu
85 90 95

Gly Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu
100 105 110

Ala Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asp
115 120 125

Ile Gln Thr Val Glu Lys Leu Ile Leu Asn Trp Tyr Gln Thr Arg Leu
130 135 140

Asp Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu

145 150 155 160

Gln Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Thr Tyr Leu Val
 165 170 175

Val Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys
 180 185 190

Gln Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg
 195 200 205

Arg Lys Ala Glu Gln Ala Ala Ala Glu Gln Ala Leu Lys Lys Leu Glu
 210 215 220

Leu Glu
 225

<210> 7
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 7

His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser
 1 5 10

<210> 8
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 <223> Synthetic

<400> 8
 atccctttct tccgcatgtg 20

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 9
 gccaaaggcgt gacatgatat 20

<210> 10

<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 10
cggatcatta aagagcaagc

20

<210> 11
<211> 20
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<213> Artificial Sequence
<220>
<223> Synthetic

<400> 11
tattcaccaa agagcttcgc

20

<210> 12
<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 12
caatcgtgga aagaagcaga

20

<210> 13
<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 13
gctcccatTT cgccttgctg

20

<210> 14
<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 14
atgctctctt tcccaccta

20

<210> 15
<211> 20
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<213> Artificial Sequence
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<400> 15
aaataactcca cacttgcacg 20

<210> 16
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<213> Artificial Sequence
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<400> 16
tgcacattca ccaaagtcac 20

<210> 17
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<223> Synthetic

<400> 17
agtctagggt cacaatctgg 20

<210> 18
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<400> 18
ttcagttgta gtggtccgac 20

<210> 19
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<213> Artificial Sequence
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<400> 19
caaggcacgc ctctcagatc gctagagaag gcttttctca 40

<210> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 20

cattaattct cgcagctagc gctgcgttct tcatcgacgc

40

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 21

ccaaatactg atcgacaact tattgaaaact tctcc

35

<210> 22

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 22

gagtttgaag aagcaattgg agtaattttt actcatg

37

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 23

tcgacttctg gcaagggcat tcacatt

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<210> 24

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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cctctgtgcc agcttctgtt tgtcag

26

<210> 25

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 25
tgtcagtttg tttgactttg ggacta

26

<210> 26
<211> 26
<212> DNA
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<220>
<223> Synthetic

<400> 26
tttgctagga ggtggcgaag tttcac

26

<210> 27
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<400> 27
gcttgatggc ctcttctcca ggataaatgc

30

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence
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<400> 28
aatgctgtgc ctaattcctg tgcgtcttgc

30

<210> 29
<211> 48
<212> DNA
<213> Artificial Sequence
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<400> 29
caggtgctgt cctcatcaga ctcacactcg gattcactgg aactctct

48

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence
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<400> 30
cactgggcag gaaagaacta gggttg

26

<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 31
 tggaaactat taaaactggg aggtgg

26

<210> 32
 <211> 50
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 32
 aggcattggag ggagggggca tcatgaagg gaaagtgcct tgtccaggag

50

<210> 33
 <211> 40
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 33
 caaggcacgc ctctcagatc gctagagaag gcttttctca

40

<210> 34
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 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 34
 cattaattct cgcagctagc gctgcgttct tcatcgacgc

40

<210> 35
 <211> 20
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 <213> Homo sapiens
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Cys Arg Ser Asp Tyr Asp Arg Gly Arg Thr Pro Ser Arg His Arg Ser
 1 5 10 15

Tyr Glu Arg Ser

<210> 36
 <211> 20
 <212> PRT
 <213> Homo sapiens
 <400> 36

Cys Arg Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu
 1 5 10 15

Asp Ile Lys Lys
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<210> 37
 <211> 466
 <212> PRT
 <213> Homo sapiens
 <400> 37

Asn Pro Asp His Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln
 1 5 10 15

Pro Lys Tyr Gly Asp Arg Lys Val His His Met His Met Arg Lys Lys
 20 25 30

Gly Ile Asn Thr Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp
 35 40 45

Pro Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly
 50 55 60

Asp Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe
 65 70 75 80

Pro Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val
 85 90 95

Gln Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro
 100 105 110

Phe Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu
 115 120 125

Arg His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr
 130 135 140

Leu Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu
 145 150 155 160

Phe Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His
 165 170 175

Pro Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr
 180 185 190

Ser Pro Val Leu Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val
 195 200 205

Ile Phe Thr His Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr
 210 215 220

Val Gly Phe Asn His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe
 225 230 235 240

Leu Gly Asp Ser Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile
 245 250 255

His Phe Pro Asp His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser
 260 265 270

Leu Val Asn Asn Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met
 275 280 285

Gln Glu Tyr Ala Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu
 290 295 300

Arg Thr Lys Thr Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu
 305 310 315 320

Tyr Thr Asp Lys Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys
 325 330 335

Phe Phe Pro Arg Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp
 340 345 350

Pro Lys Ser Gln Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly
 355 360 365

Lys Glu Pro Asp Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro
370 375 380

Ser His Ala Arg Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg
385 390 395 400

Ile Gly Cys Gly Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala
405 410 415

Ala Met Asp Ala Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln
420 425 430

Lys Arg Phe Ile Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg
435 440 445

Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile
450 455 460

Lys Lys
465